-continued

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TAAGCTTGGG AATCATCTCG CCGACGGGCA GCGATATGGG CATCATGCTC GCCCCGCCCC 60

AATCCTCGAA GAATAGTGCA ATAATGCAAA CGATATCACC CCAGCAACAG CAGCAGCAGC 120

AGCAGCAGCA ACAGCAGCAA CATCAGCAGC AGCAACAGCA GCAGCAACAG CAGCAGCAGC 180

AACAGCAGCA GCAACTCGGA GGCCTGGAGT TCGGTTCAGA GGGCTTGGAC CTGAATGGAT 240

TTTGTGGATC TCCGGGTAAG TGGTCACTCA TGATGGACTC TATGGACTCG CTAACTAGCT 300

AACTAATCAT TCTACCATCC CAACTTGCAG ACTCATTTCA CTCGGGTCAA ATGAATCCGC 360

CCTCGATACA AAGTTCAAT 379

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: repeat_region
(B) LOCATION: 58..87
(D) OTHER INFORMATION: /rpt_type= "other"
/label= tg_DINUCLEOTIDE

(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 58..87
(D) OTHER INFORMATION: /label= TG_DINUCLEOTIDE
/note= "THIS STRETCH OF TG DINUCLEOTIDES RANGES IN SIZE FROM 15 DINUCLEOTIDES TO 25 DINUCLEOTIDES ((TG)15 TO 25)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTCCCCCACA CAAAGAAGTT CTGTTCTCTT CCCTCTACCT TGATGAATGC ACTGTGATGT 60

GTGTGTGTGT GTGTGTGTGT GTGTGTGACT CGTTCCCAGG TATGGAA 107

We claim:

1. A method for determining length polymorphisms in a simple or cryptically simple sequence in one or more DNA regions of one or more subjects, which comprises:

a) providing at least one DNA sample, comprising a template DNA having a nucleotide sequence that includes a simple or cryptically simple sequence *comprising trinucleotide repeats*, from at least one subject;

b) annealing at least one primer pair to the template DNA of each of said DNA samples, wherein said primer pair is composed of a first primer complementary to a nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 5' side of said simple or cryptically simple DNA sequence and a second primer complementary to a nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 3' side of said simple or cryptically simple DNA sequence; wherein said first and second primers each anneal to a single site in said template DNA and the sequence of the template DNA between the sites where said primers anneal is 50 to 500 nucleotides in length;

c) performing at least one primer-directed polymerase chain reaction upon said template DNA having said primers annealed thereto, so as to form at least one polymerase chain reaction product;

d) separating the products of each polymerase chain reaction according to their lengths; *and*

e) analyzing the *lengths of the* separated products to determine the length polymorphisms of the simple or cryptically simple sequences.

[2. The method according to claim **1**, wherein each simple or cryptically simple DNA sequence comprises at least one trinucleotide motif.**]**